

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 22, 2003, 14:09:12 ; Search time 33 Seconds

(without alignments)
4426.210 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 506

Sequence: 1 GTGATGTACTTACTGTGCTCTGTACTTAACATCA 1553

Scoring table:

	OLIGO	Xgapop 60.0	Xgapext 60.0
Xgapop	60.0	Xgapext 60.0	
Fgapop	6.0	Fgapext 7.0	
Delop	6.0	Delext 7.0	

Searched: 127863 seqs, 47026705 residues

Word size: 1

Total number of hits satisfying chosen parameters: 255550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPRO/US09745506/runat_22082003_132737_11173/app.query.fasta.1.1735
-DB=SwissProt_41 -QFMT=fastan -SUFFIX=n2poli.rsp -MINMATCH=0.1 -LOOPEL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=fto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09745506.ecgn.1.1.40.etrnat.22082003_132737_11173 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350	69.2	350	NEFL_HUMAN	O9qzt8 homo sapien
2	51	10.1	350	NEFL_MOUSE	O9qzt8 mus musculu
3	10	2.0	350	YF59_STAMM	O99ct7 staphylococ
4	9	1.8	288	NIF3_YEAST	P53081 saccharomyc
5	8	1.6	169	E1BS_ADECG	O65942 canine aden
6	8	1.6	169	E1BS_ADECG	P35984 canine aden
7	8	1.6	169	E1BS_ADECR	O96078 canine aden
8	8	1.6	367	CCR3_MOUSE	O88810 mus musculu
9	8	1.6	368	CCR3_HUMAN	P49682 homo sapien
10	8	1.6	655	MAL1_MOUSE	P45700 mus musculu
11	8	1.6	1440	POLG_JAEVN	P14403 j genome po
12	8	1.6	1490	CDRA_CANAL	O74676 candida alb
13	8	1.6	1664	RPAL_YEAST	P10964 saccharomyc
14	8	1.6	1689	RPAL_SCHRO	P15398 schizosach
15	8	1.6	1780	POLG_AVEV	P05769 m genome po
16	8	1.6	3432	POLG_JAEVS	P19110 j genome po
17	7	1.4	81	UCRO_HUMAN	O14949 homo sapien
18	7	1.4	81	UCRO_MOUSE	O9c969 mus musculu

19	7	1.4	119	1	RNPA_MYCPA	O91719 mycobacteri
20	7	1.4	122	1	PC32_CLAPU	P22371 claviceps p
21	7	1.4	134	1	VG32_HSV1	O00100 ictalurids h
22	7	1.4	137	1	ERV4_YEAST	P53173 saccharomyc
23	7	1.4	146	1	RL28_TRYCR	O00822 trypanosoma
24	7	1.4	146	1	SSBS_XENLA	P09380 xenopus lae
25	7	1.4	148	1	SSBR_XENLA	P09381 xenopus lae
26	7	1.4	150	1	COXA_HUMAN	P20674 homo sapien
27	7	1.4	152	1	MGSA_PASMO	O9c9n3 pasteurella
28	7	1.4	165	1	Y05B_CAEEL	O09254 caenorhabdi
29	7	1.4	165	1	CGH8_HUMAN	P01233 homo sapien
30	7	1.4	165	1	PSAF_SYNY3	P29256 synecocyst
31	7	1.4	173	1	NUG6_ONCMY	P48177 oncorhynch
32	7	1.4	173	1	NUG6_SALSA	O92zm2 salmo salar
33	7	1.4	177	1	IL10_SHEEP	O29408 ovls aries
34	7	1.4	188	1	AMPK_METFE	P22624 methanother
35	7	1.4	197	1	DCR1_RHOCA	P37740 rhodobacter
36	7	1.4	198	1	NGAL_RAT	P30152 rattus norv
37	7	1.4	198	1	SDC4_MOUSE	O35988 mus musculu
38	7	1.4	201	1	NUG6_CYACA	P48925 cyanidium c
39	7	1.4	211	1	IPYR_SOLITU	O43187 solanum tub
40	7	1.4	218	1	Y279_MYCCE	P47521 mycoplasma
41	7	1.4	221	1	IFR3_ARATH	O9fks9 arabidopsis
42	7	1.4	221	1	PSB1_ORYSA	O64464 oryza sativ
43	7	1.4	224	1	FLGA_YEREN	O56992 yersinia en
44	7	1.4	224	1	MYOG_HUMAN	P15173 homo sapien
45	7	1.4	224	1	MYOG_MOUSE	P12979 mus musculu

ALIGNMENTS

RESULT 1

NEFL_HUMAN
ID NEFL_HUMAN STANDARD: PRT: 350 AA.

AC O9GZT8; Q9H2D2; Q9HC18;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE NIF3-like protein 1 (Amphotropic lateral sclerosis 2 chromosomal

region candidate gene protein 1) (Myo18 protein) (MDS015).

GN NIF3L1 OR ALS2CR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.

RX MEDLINE-20573864; PubMed-11124544;

RA Tascou S., Uedelhoven J., Dixkens C., Neyerla K., Engel W.,

RA Burfeind P.;

RT "Isolation and characterization of a novel human gene, NIF3L1, and its

RT mouse ortholog, Nif3l1, highly conserved from bacteria to mammals."

RL Cytogenet. Cell Genet. 90:330-336(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-21100893; PubMed-11161814;

RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,

RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,

RA Ikeda J.-E., Hayden M.R.;

RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,

RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)

RT critical region at chromosome 2q33-q34: candidate genes for ALS2."

RL Genomics 71:200-213(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Mao Y.M., Xie Y., Huang X.Y., Ying K., Dai J.L.;

RA Submitted (Apr-1998) to the EMBL/Genbank/DDJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z.;

RT "Novel genes expressed in hematopoietic stem/progenitor cells from

RT myelodysplastic syndromes patient."

AC Q9EQ80; Q9D098;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NIF3-like protein 1.
 GN NIF3L1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=20573864; PubMed=1124544;
 RA Tascos S., Uedelhoven J., Dixkens C., Nayeria K., Engel W.,
 RA Burfelind P.;
 RT "Isolation and characterization of a novel human gene, NIF3L1, and its
 RL mouse ortholog, Nif3l1, highly conserved from bacteria to mammals.";
 RL Cytogenet. Cell Genet. 90:330-336(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kocichwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofman M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombarits P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF284439; BAAG5961.1; ALT_INIT.
 DR EMBL; AK011670; BAB27769.1; ALT_INIT.
 DR MGD; MGI:1929485; Nif3l1.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1.
 DR TIGRfams: TIGR00486; 1.
 FT CONFLICT 164 164 G -> S (IN REF. 2).
 FT CONFLICT 178 178 E -> K (IN REF. 2).
 FT CONFLICT 191 191 L -> F (IN REF. 2).
 FT CONFLICT 195 195 L -> O (IN REF. 2).
 FT CONFLICT 198 198 L -> F (IN REF. 2).
 FT CONFLICT 208 208 T -> I (IN REF. 2).
 SQ SEQUENCE 350 AA; 38828 MW; B0FA71503FCF086 CRC64;

Alignment Scores:
 Pred. No.: 5, 71e-44 Length: 350
 Score: 51.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.08% Indels: 0
 DB: 1 Gaps: 0
 US-09-745-506-74 (1-1553) x NIF3L_MOUSE (1-350)
 QY 245 ATGATTTGAGAGCGCTCCCTTCCTTCCTGTAATGACTTCATCCCTCGTTGCTGAG 304
 DB 1 MetaspLeuLyAlaLeuLeuSerSerLeuAaAnSpPheAlaSerLeuSerPheAlaGlu 20
 QY 305 AGTTGGACAAATGTTGGATTACTGCTGGACCAAGCCGACCATCTCTAAATACAC 364
 DB 21 SerrTPasPasVaIcIlyLeuLeuValGluProSerProProHisThrValaSnThrLeu 40
 QY 365 TTCCTGACCAATGACTGCTGAGGAGGATG 397
 DB 41 PheLeuThrAsnAspLeuThrGluGluValMet 51
 RESULT 3
 YF59_STAM STANDARD; PRT; 366 AA.
 ID YF59_STAM
 AC 099TT7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein SAV1559/SA1388.
 GN SAV1559 OR SA1388.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino T., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Katto C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuuchi J.,
 RA Kanihisa K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RL aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
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 CC -----
 DR EMBL; AP003362; BAB57721.1; -;
 DR EMBL; AP003134; BAB42651.1; -;
 DR PIR: F89936; F89936.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; NIF3; 1.
 DR TIGRfams: TIGR00486; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 366 AA; 41075 MW; CA7D5FADF87FF4 CRC64;

Alignment Scores:
 Pred. No.: 0.158 Length: 366
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.98% Indels: 0
 DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x YF59_STAM (1-366)

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OY 239 GCTGAGAGTGGACATGTTGATTACG 328
DB 19 AlaGUSerTPpASpAShValcIyLeuLeu 28

RESULT 4
NIF3_YEAST STANDARD: PRT: 288 AA.
ID NIF3_YEAST
AC P53081:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN NGG1-interacting factor 3.
OS NIF3 OR YGL221C.
OC Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=97435481; PubMed=9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT chromosome VII.";
RL Yeast 13:1077-1090(1997).
CC -1 SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
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CC -----
DR EMBL: Z72743; CAA96937.1;
DR PIR: S64243; S64243.
DR SGD: S0003189; NIF3.
DR InterPro: IPR002678; DUF34.
DR Pfam: PF01784; NIF3; 1.
DR TIGRfams: TIGR00486; TIGR00486; 1.
SQ SEQUENCE 288 AA; 3188 MW; B6AB6E4BAFA4776A CRC64;

Alignment Scores:
Pred. No.: 1.77 Length: 288
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.78% Indels: 0
Gaps: 0
DB: 1

US-09-745-506-74 (1-1553) x NIF3_YEAST (1-288)
OY 1178 CACAGCAGACGTGACGAGGCTTCTT 1204
DB 252 HisSerAnThrGluArgGlyPheLeu 260

RESULT 5
EIBS_ADECC STANDARD: PRT: 169 AA.
ID EIBS_ADECC
AC Q65942;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE E1B protein, small T-antigen (Early E1B 19 kDa protein).
OS Canine adenovirus type 1 (strain CL1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=69150;
RN [1]
RP SEQUENCE FROM N.A.
RC Campbell J.B., Zhao Y.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL: U55001; AAB05430.1;
DR InterPro: IPR002924; AdenoE1B_19kDa.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF01691; AdenoE1B_19k; 1.
DR ProDom: PD004074; AdenoE1B_19kDa; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Early protein.
SQ SEQUENCE 169 AA; 19333 MW; F8A4DC68B8D0DFE4 CRC64;

Alignment Scores:
Pred. No.: 20.6 Length: 169
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
Gaps: 0
DB: 1

US-09-745-506-74 (1-1553) x EIBS_ADECC (1-169)
OY 1384 CTTCCAGAGAGTGTCTTCGAGGT 1407
DB 138 LeuProGUSerValPheGluGly 145

RESULT 6
EIBS_ADECC STANDARD: PRT: 169 AA.
ID EIBS_ADECC
AC P35984;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE E1B protein, small T-antigen (Early E1B 19 kDa protein).
OS Canine adenovirus type 1 (strain Glaxo).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10513;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90163565; PubMed=2623943;
RA Spibey N., McCleary R.S., Cavanagh R.M.A.;
RT "Identification and nucleotide sequence of the early region 1 from
RT canine adenovirus types 1 and 2.";
RL Virus Res. 14:241-256(1989).
DR PIR: C60010; C60010.
DR InterPro: IPR002924; AdenoE1B_19kDa.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF01691; AdenoE1B_19k; 1.
DR ProDom: PD004074; AdenoE1B_19kDa; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Early protein.
SQ SEQUENCE 169 AA; 19364 MW; 4B7F31A74136623F CRC64;

Alignment Scores:
Pred. No.: 20.6 Length: 169
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
Gaps: 0
DB: 1

US-09-745-506-74 (1-1553) x EIBS_ADECC (1-169)
OY 1384 CTTCCAGAGAGTGTCTTCGAGGT 1407
DB 138 LeuProGUSerValPheGluGly 145

RESULT 7

```

EIBS_ADECR
ID EIBS_ADECR STANDARD: PRT: 169 AA.
AC 096678;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE E1B protein, small T-antigen (Early E1B 19 kDa protein).
OS Canine adenovirus type 1 (strain R1261).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=69151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97275900; PubMed=9129661;
RA Morrison M.D., Onions D.E., Nicolson L.;
RT *Complete DNA sequence of canine adenovirus type 1.*;
RL J. Gen. Virol. 78:873-878(1997).
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CC
CC EMBL: Y07760; CAA69053.1;
DR InterPro: IPR002924; AdenoE1B_19kDa.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF01691; Adeno_E1B_19kDa; 1.
DR ProDom: PD004074; AdenoE1B_19kDa; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Early protein.
SQ SEQUENCE 169 AA; 19367 MW; F8A4D2868ED0FE4 CRC64;

Alignment Scores:
Pred. No.: 20.6 Length: 169
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x EIBS_ADECR (1-169)
QY 1384 CTTCCAGAGAGTGTTCGAGGCT 1407
DB 138 LeuProGluSerValPheGluGly 145

RESULT 8
ID CCR3_MOUSE STANDARD: PRT: 367 AA.
AC 088410;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3).
GN CXCR3 OR CMKAR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98318636; PubMed=9653165;
RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Hedrick J., Zlotnik A.;
RT The CC chemokine 6CKine binds the CXC chemokine receptor CXCR3.*;
RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
CC -1- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC (BY
CC SIMILARITY). BINDS TO SCYB21.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF045146; AAC40163.1;
DR MGI: MGI:1277207; Cxcr3.
DR InterPro: IPR004070; CXC_chemkine3.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01532; CXCR3_KINER3.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP_FL1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52
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FT DISULFID 123 202
FT CARBOHYD 22 22
FT CARBOHYD 32 32
SQ SEQUENCE 367 AA; 41016 MW; 029FB778E3CD4EA CRC64;

Alignment Scores:
Pred. No.: 18.6 Length: 367
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x CCR3_MOUSE (1-367)
QY 744 TCACCTCTTTTCTGCTAGACTG 767
DB 60 SerLeuLeuPheLeuGluGlyLeu 67

RESULT 9
ID CCR3_HUMAN STANDARD: PRT: 368 AA.
AC P49682; O15185;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3) (CD183
DE antigen).
GN CXCR3 OR GPR9.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RX MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,
RA Clark-Lewis I., Baggiolini M., Moser B.;
RT "Chemokine receptor specific for IP10 and mlg: structure, function,

RT and expression in activated T-lymphocytes.";
J. Exp. Med. 184:963-969(1996).
[2]
SEQUENCE FROM N.A.
RA Gutierrez J., Varona R., Zaballero A., Lind P., Marquez G.;
submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC TISSUE-BRAIN, Lung, and Testis;
MEDLINE-22388257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatcenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Scheetz T.E.,
Brownstein M.J., Umed T.B., Toshlyuk S., Carantini P., Prange C.,
Raba S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 5-368 FROM N.A.
MEDLINE-96115583; PubMed-8666380;
RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
O'Dowd B.F., Docherty J.M.;
"Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
and GPR14, encoding receptors related to Interleukin 8, neuropeptide
Y, and somatostatin receptors.";
Genomics 29:335-344(1995).
[5]
LIGAND BINDING.
RC TISSUE-Fetal astrocytes;
MEDLINE-98290735; PubMed-9625760;
RA Cole K.E., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
Neote K.;
"Interferon-inducible T cell alpha chemottractant (I-TAC): A novel
non-ELR CXC chemokine with potent activity on activated T cells
through selective high affinity binding to CXCR3.";
J. Exp. Med. 187:2009-2021(1998).
[6]
-1- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP1 AND SCYB11/ITAC.
[7]
-1- SUBCELLULAR LOCATION: Integral membrane protein.
[8]
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
[9]
-1- DATABASE: NAME=PROX; NOTE=PROX 1:78-83(2000).
[10]
WWW="http://www.ncbi.nlm.nih.gov/prox/guide/650534941_g.htm".
[11]
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[12]
CC EMBL: X95876; CAAG5126.1; -;
DR EMBL: X95876; CAB02143.1; ALT_INT.
DR EMBL: BC034403; AAH34403.1; -;
DR EMBL: U32674; AAC30505.1; -;
DR Genew: HGNC:4540; CXCR3.
DR MIM: 600894; -;
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DR GO: GO:0005887; C:Integral to plasma membrane; TAS.

DR GO: GO:0006960; P:antimicrobial humoral response (sensu Inver. . .); TAS.
DR GO: GO:0007155; P:cell adhesion; TAS.
DR GO: GO:0006928; P:cell motility; TAS.
DR GO: GO:0006935; P:chemotaxis; TAS.
DR GO: GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR InterPro: IPR004070; CXC_chemkine3.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01532; CXCCHRMNERS.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS02624; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Antigen.
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FT TRANSMEM 20650
FT TRANSMEM 20671
FT TRANSMEM 20692
FT TRANSMEM 20713
FT TRANSMEM 20734
FT TRANSMEM 20755
FT TRANSMEM 20776
FT TRANSMEM 20

CC oligosaccharides. Progressively trim alpha-1,2-linked mannose
 CC residues from Man(9)GLCNAC(2) to produce Man(5)GLCNAC(2).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the terminal 1,2-linked alpha-D-
 CC mannose residues in the oligo-mannose oligosaccharide
 CC Man(9)(GLCNAC)(2).
 CC -1- COFACTOR: Calcium.
 CC -1- ENZYME REGULATION: Inhibited by both 1-deoxymannojirimycin and
 CC kifunensine (By similarity).
 CC -1- PATHWAY: N-GLYCOSYLATION.
 CC -1- SUBUNIT: BELONGS TO FAMILY 47 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 DR EMBL: U04299; AAA17747.1; -
 DR PIR: A54408; A54408.
 DR HSSP: P32906; IDL2.
 DR MGD: MGI:104677; Man1a.
 DR GO: GO:0000139; C:Golgi membrane; IDA.
 DR InterPro: IPR001382; Glyco_hydro_47.
 DR Pfam: PF01532; Glyco_hydro_47; 1.
 DR PRINTS: PR00747; GLYHDRLASE47.
 DR PRODOM: PD003239; Glyco_hydro_47; 1.
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane; Calcium-binding;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 44 64 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL (POTENTIAL).
 FT CA_BIND 271 282 POTENTIAL.
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 655 AA; 73375 MW; 15AF658364930B84 CRC64;
 Alignment Scores:
 Pred. No.: 17.2 Length: 655
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.58% Indels: 0
 DB: 1 Gaps: 0
 US-09-745-506-74 (1-1553) x M1A1_MOUSE (1-655)
 QY 487 GAAGAGCGCGCTGTGATCCGGCG 510
 ||||||||||||||||||
 Db 109 GUGUGYALAPROGLYASPROGLY 116
 RESULT 11
 ID POLG_JAEVN STANDARD; PRT; 1440 AA.
 AC P14403; P08769; .
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Genome polypeptide [Contains: Capsid protein C (Core protein); Matrix
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural
 DE proteins NS1, NS2A, and NS2B; Protease/helicase (EC 3.4.21.98) (NS3)]
 DE (Fragment).
 OS Japanese encephalitis virus (strain Nakayama).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=67236200; PubMed=3035787;
 RA McAda P.C., Mason P.W., Schmaljohn C.S., Dalrymple J.M., Mason T.L.,
 Fournier M.J.;

RT "Partial nucleotide sequence of the Japanese encephalitis virus
 RT genome.";
 RL . Virolgy 158:348-360(1987).
 CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
 CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
 CC precursor polypeptide, commonly with Asp or Glu in the P6
 CC position, Cys or Thr in P1 and Ser or Ala in P1'.
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
 CC PROTEIN C AND RNA.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M16574; AAA46251.1; -
 DR PIR: A27844; GNMVJF.
 DR HSSP: P14336; 1SVB.
 DR InterPro: IPR001122; Flavi_glycoprote.
 DR InterPro: IPR000336; Flavi_glycoprote.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR001157; Flavi_NS1.
 DR InterPro: IPR000752; Flavi_NS2A.
 DR InterPro: IPR000487; Flavi_NS2B.
 DR InterPro: IPR002535; Flavi_propep.
 DR Pfam: PF01003; Flavi_capsid; 1.
 DR Pfam: PF02832; Flavi_glycop_C; 1.
 DR Pfam: PF00869; Flavi_glycoprot; 1.
 DR Pfam: PF01004; Flavi_M; 1.
 DR Pfam: PF00948; Flavi_NS1; 1.
 DR Pfam: PF01005; Flavi_NS2A; 1.
 DR Pfam: PF01002; Flavi_NS2B; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR PRODOM: PD001556; Flavi_glycoprote; 1.
 DR PRODOM: PD001496; Flavi_NS1; 1.
 KW Polypeptide; Glycoprotein; Core protein; Coat protein;
 KW Envelope protein; Hydrolyase; Helicase; ATP-binding; Transmembrane;
 KW Nonstructural protein 1.
 FT NON_TER 1 53 CAPSID PROTEIN C.
 FT CHAIN 1 54
 FT PROPEP 54 146
 FT CHAIN 147 222
 FT CHAIN 223 794
 FT CHAIN 795 1136
 FT CHAIN 1137 1301
 FT CHAIN 1302 1432
 FT CHAIN 1433 >1440
 FT CHAIN 1433 1440
 FT DISULFID 225 252
 FT DISULFID 282 338
 FT DISULFID 296 327
 FT DISULFID 314 343
 FT DISULFID 412 509
 FT DISULFID 526 557
 FT CARBOHYD 68 68
 FT CARBOHYD 376 376
 FT CARBOHYD 852 852
 FT CARBOHYD 929 929
 FT NON_TER 1440 1440
 SQ SEQUENCE 1440 AA; 158184 MW; 4D489A365A3C2B6E CRC64;
 Alignment Scores:
 Pred. No.: 15.5 Length: 1440
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.58% Indels: 0

DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x POLG_JAEVN (1-1440)

QY 1056 GTGCTGTTCTGGAGACAGCTTC 1079
 |||||||
 DB 1180 ValLeuValLeuGlyAlaAlaPhe 1187

RESULT 12

CDR4_CANAL STANDARD: PRT; 1490 AA.

AC 074676;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ABC transporter CDR4.
 GN CDR4.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=1161;
 RX MEDLINE=98440373; PubMed=9767132;
 RA Franz R., Michel S., Morschhauser J.,
 RT "A fourth gene from the Candida albicans CDR family of ABC
 RT transporters";
 RL Gene 220:91-98(1998).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDS SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF044921; AAC72295.1; -
 DR PIR; T30550; T30550.
 DR InterPro: IPR003439; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR005285; PDR.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR TIGRFAMs; TIGR00956; 3a01205; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding; Transmembrane; Glycoprotein; Transport; Repeat.
 FT DOMAIN 1 516
 FT TRANSMEM 517 537 POTENTIAL.
 FT TRANSMEM 551 571 POTENTIAL.
 FT TRANSMEM 601 621 POTENTIAL.
 FT TRANSMEM 626 646 POTENTIAL.
 FT TRANSMEM 659 679 POTENTIAL.
 FT TRANSMEM 767 787 POTENTIAL.
 FT DOMAIN 1182 1183 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1183 1203 POTENTIAL.
 FT TRANSMEM 1217 1237 POTENTIAL.
 FT TRANSMEM 1268 1288 POTENTIAL.
 FT TRANSMEM 1304 1324 POTENTIAL.
 FT TRANSMEM 1333 1353 POTENTIAL.
 FT TRANSMEM 1455 1475 POTENTIAL.
 FT NP_BIND 882 889 ATP (POTENTIAL).
 SQ SEQUENCE 1490 AA; 169341 MW; 858676C872A4F5C5 CRC64;

Alignment Scores:

Pred. No.: 15.4 Length: 1490
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.61% Indels: 0

DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x CDR4_CANAL (1-1490)

QY 1028 CTAAAGTTCTCCCAACCCCAAGG 1005
 |||||||
 DB 1395 LeuArgPheSerProProGingly 1402

RESULT 13

RPAL_YEAST STANDARD: PRT; 1664 AA.

AC P10964; Q99330;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6) (A190).
 GN RPAL OR RPAL90 OR RRL OR YOR341W OR O6276.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 [1]
 RN RP SEQUENCE FROM N.A.
 RC MEDLINE=88139333; PubMed=2830265;
 RA Memet S., Gouy M., Marck C., Sentenac A., Buhler J.-M.,
 RT "RPAL90, the gene coding for the largest subunit of yeast RNA
 RT polymerase A.";
 RL J. Biol. Chem. 263:2830-2839(1988).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=5288c / FY73;
 RX MEDLINE=97103776; PubMed=8948102;
 RA Purnelle B., Goffeau A.;
 RT "Nucleotide sequence analysis of a 40 kb segment on the right arm of
 RT private chromosome XY reveals 18 open reading frames including a new
 RL yeast 12.14/5-1481(1996)."
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
 CC RIBOSOMAL DNA UNITS.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
 CC (RNA)(n).
 CC -1- SUBUNIT: RNA POLYMERASE I CONSISTS OF 14 DIFFERENT SUBUNITS. THIS
 CC SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE I.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE
 CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
 CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
 CC III FOR 5S AND TRNA GENES.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; J03530; AAA34890.1; -
 DR EMBL; X95720; CAA65029.1; -
 DR EMBL; 275249; CAA99665.1; -
 DR PIR; S67250; S67250.
 DR SGD; S0005868; RPA190.
 DR InterPro: IPR000722; RNA_pol_A.
 DR InterPro: IPR007080; RNA_pol_Rp1.1.
 DR InterPro: IPR007066; RNA_pol_Rp1.3.
 DR InterPro: IPR007083; RNA_pol_Rp1.4.
 DR InterPro: IPR007081; RNA_pol_Rp1.5.
 DR InterPro: IPR006593; RNA_pol_A_N.
 DR Pfam; PF04997; RNA_pol_Rp1.1; 1.

DR Pfam: PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam: PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam: PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam: PF04988; RNA_pol_Rpb1_5; 1.
 DR SMART; SM00663; RPOA_N; 1.
 KW Transferrase; DNA-directed RNA polymerase; Transcription; zinc;
 ZNc-finger; Nuclear protein.
 FT ZNc-FING 62 78 C2H2-TYPE (POTENTIAL).
 FT CONFLICT 158 158 N -> T (IN REF. 1).
 SQ SEQUENCE 1664 AA; 186431 MW; DF65A7AA59D5E6D CRC64;

Alignment Scores:
 Pred. No.: 15.2 Length: 1664
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.61% Indels: 0
 DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x RPA1_YEAST (1-1664)

OY 591 TPAGCAACGAGTGTGACGCC 568
 DB 557 LeuAlaSmcInLeuLeuTrPro 564

RESULT 14
 RPA1_SCHPO STANDARD; PRT; 1689 AA.

AC P15398;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6).
 GN RPA1 OR NUCL OR SPBC4C3.05C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_Taxid=4896;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139548; PubMed=2537310;
 RA Hirono T., Konoha G., Toda T., Yanagida M.;
 RT "Essential roles of the RNA polymerase I largest subunit and DNA
 RT topoisomerases in the formation of fission yeast nucleolus.";
 RL J. Cell Biol. 108:243-253(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX STRAIN=972; HMI23;
 RA MEDLINE=89232741; PubMed=2854522;
 RA Yamagishi M., Nomura M.;
 RT "Cloning and sequence determination of the gene encoding the largest
 RT subunit of the fission yeast Schizosaccharomyces pombe RNA polymerase
 RT I.";
 RL Gene 74:503-515(1988).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Osell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckart G., Bert R., Robben J., Gymnopoulos B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Beer P., Zimmermann W., Medler H., Wambut R., Pinnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Motter S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucan M., Rochet M., Galliard C., Tallade V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakowski G.V., Usery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
 CC RIBOSOMAL DNA UNITS.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -1- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
 CC DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
 CC RNA POLYMERASE I.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE
 CC FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
 CC PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
 CC III FOR 5S AND TRNA GENES.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: X14783; CA32887.1; -;
 DR EMBL: M37411; AAA35326.1; -;
 DR EMBL: A1021730; CAA16827.1; -;
 DR PIR: JS0080; JS0080.
 DR Genedb_Spombe: SPBC4C3.05C; -;
 DR InterPro: IPR000722; RNA_pol_A.
 DR InterPro: IPR007080; RNA_pol_Rpb1_1.
 DR InterPro: IPR007066; RNA_pol_Rpb1_3.
 DR InterPro: IPR007083; RNA_pol_Rpb1_4.
 DR InterPro: IPR007081; RNA_pol_Rpb1_5.
 DR InterPro: IPR006592; RNA_POLA_N.
 DR Pfam: PF04997; RNA_pol_Rpb1_1; 1.
 DR Pfam: PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam: PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam: PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam: PF04988; RNA_pol_Rpb1_5; 1.
 DR SMART; SM00663; RPOA_N; 1.
 KW Transferrase; DNA-directed RNA polymerase; Transcription; zinc;
 ZNc-finger; Nuclear protein.
 FT ZNc-FING 63 79 C2H2-TYPE (POTENTIAL).
 FT CONFLICT 69 69 D -> A (IN REF. 1).
 FT CONFLICT 84 84 T -> S (IN REF. 1).
 FT CONFLICT 704 704 T -> I (IN REF. 1).
 FT CONFLICT 1581 1581 A -> T (IN REF. 1).
 FT CONFLICT 1681 1681 T -> N (IN REF. 1).
 SQ SEQUENCE 1689 AA; 189244 MW; 2D2D3A2DEC94A497 CRC64;

Alignment Scores:
 Pred. No.: 15.2 Length: 1689
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.61% Indels: 0
 DB: 1 Gaps: 0

US-09-745-506-74 (1-1553) x RPA1_SCHPO (1-1689)

QY 591 TTAGCACCAGTTGTTGACGCC 568
 |||||
 Db 565 LeuAlaAsnGlnLeuThrPro 572

RESULT 15
 POLG_MVEV STANDARD; PRT; 1780 AA.
 AC P05769;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 40, Last annotation update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Genome polypeptide (Contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2A, and NS2B; Protease/helicase (PC 3.4.21.98) (NS3)) (Fragment).
 DE Murray valley encephalitis virus.
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 NC NCBI_TaxID=11079;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86200215; PubMed=3009829;
 RA Daigarno L., Trent D.W., Strauss J.R., Rice C.M.;
 RT "Partial nucleotide sequence of the Murray Valley encephalitis virus genome. Comparison of the encoded polypeptides with yellow fever virus structural and non-structural proteins.";
 RL J. Mol. Biol. 187:309-323(1986).
 CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS2A AND NS2B MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polypeptide, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
 CC
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 CC
 DR EMBL: X03467; CAA27184.1;
 DR PIR: A24635; GMYVMV.
 DR HSSP: PL4336; ISVB.
 DR MEROPS: S07.001;
 DR InterPro: IPR001122; Flav1_capsidC.
 DR InterPro: IPR000336; Flav1_glycoprote.
 DR InterPro: IPR001850; Flav1_helicase.
 DR InterPro: IPR000069; Flav1_M.
 DR InterPro: IPR001157; Flav1_NS1.
 DR InterPro: IPR000752; Flav1_NS2A.
 DR InterPro: IPR000487; Flav1_NS2B.
 DR InterPro: IPR002535; Flav1_propep.
 DR Pfam: PF02832; Flav1_glycopC; 1.
 DR Pfam: PF00869; Flav1_glycoprote; 1.
 DR Pfam: PF00949; Flav1_helicase; 1.
 DR Pfam: PF01004; Flav1_M; 1.
 DR Pfam: PF00948; Flav1_NS1; 1.
 DR Pfam: PF01005; Flav1_NS2A; 1.
 DR Pfam: PF01002; Flav1_NS2B; 1.
 DR Pfam: PF01570; Flav1_propep; 1.
 DR ProDom: PD001556; Flav1_glycoprote; 1.
 DR ProDom: PD001496; Flav1_NS1; 1.
 KW Polyprotein; Glycoprotein; Core protein; Coat protein;
 KW Envelope protein; Hydrolyase; Helicase; ATP-binding; Transmembrane;
 KW Nonstructural protein.
 FT INIT_MET 1 REMOVED FROM CAPSID PROTEIN C BY THE

FT CHAIN 1 121
 FT PROPEP 122 217
 FT CHAIN 218 292
 FT CHAIN 293 793
 FT CHAIN 794 1207
 FT CHAIN 1208 1372
 FT CHAIN 1373 1503
 FT CHAIN 1504 >1780
 FT CHAIN 44 60
 FT TRANSMEM 112 128
 FT TRANSMEM 278 294
 FT TRANSMEM 773 789
 FT TRANSMEM 1178 1194
 FT TRANSMEM 1219 1235
 FT TRANSMEM 1250 1266
 FT TRANSMEM 1312 1328
 FT TRANSMEM 1378 1394
 FT TRANSMEM 1401 1417
 FT TRANSMEM 1476 1492
 FT TRANSMEM 295 322
 FT DISULFID 352 408
 FT DISULFID 366 397
 FT DISULFID 384 413
 FT DISULFID 482 580
 FT DISULFID 597 628
 FT CARBOHYD 73 73
 FT CARBOHYD 140 140
 FT CARBOHYD 446 446
 FT CARBOHYD 923 923
 FT CARBOHYD 968 968
 FT CARBOHYD 1000 1000
 FT NON_TER 1780 1780
 SQ SEQUENCE 1780 AA; 194866 MW; 0D6AA7FF0EB706DE CRC64;

Alignment Scores:
 Pred. No.: 15.1
 Score: 8.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.58%
 DB: 1
 Gaps: 0

US-09-745-506-74 (1-1553) x POLG_MVEV (1-1780)

QY 1056 GTGCTGTTGCGAGACGCTTC 1079
 |||||
 Db 1251 ValLeuValLeuGlyAlaAlaPhe 1258

Search completed: August 22, 2003, 14:33:47
 Job time : 51 secs